REMARKS

The Amendments

The amendments to Claim 1 are supported in the specification by e.g.,: page 8, line 16 – page9, line 14; page 9, lines 22-23; page 10, lines 5-25; page 11, lines 5-25; page 13, lines 19-22; page 14, line 10 – page 15, line 3; figures 1 and 2.

No new matter is added in any of the above amendments. Applicants believe that the amendments address the Examiner's rejections and place the claims in a form for allowance.

The Response

The Rejections of Claims 1-16 Under § 112 Should Be Withdrawn

The Examiner has rejected claim 1 (and other claims) as unclear due to the use of the phrase "chemical genomic data." Applicants respectfully disagree and wish to direct the Examiner's attention to the specification at e.g., page 1, lines 20-23 where the term "chemical genomic annotation" is described. Further, at page 2, lines 12-16, the beginning of the "Summary of the Invention" section describes the system and methods of the invention as involving "data from chemical genomic annotation experiments."

The Examiner has rejected claims 1, 7, 10 and 12 as indefinite in the use of the terms "using" and "predicting." Applicants have deleted these terms from the amended claims thereby obviating this rejection.

The Examiner has rejected dependent claims 3, 4, 8, 9, 13, 14, 15 and 16 for lack of antecedent basis for the term "product information." Applicants have amended the corresponding independent claims and cancelled claims 13-16 thereby obviating this rejection.

The Examiner has rejected claims 10 and 12 for reciting means plus function terms that are not clearly correlated with a specific structure in the specification. Specifically, the Examiner cites the term, "means for identifying and selecting correlation information...that is useful to predict a biological activity." To the extent that the current amendments do not overcome the Examiner's rejection, Applicants respectfully disagree. Applicants assert that the specification discloses hardware and software structures that perform the function of identifying database information (e.g., displaying hyperlinked correlation information) and allows the user to select the displayed information (e.g., selecting the hyperlink). Applicants wish to specifically direct

the Examiner's attention to the specification at e.g., pages 13, line 19 – page 15, line 7, and accompanying Figures 1 and 2, for a disclosure of exemplary hardware and software structures.

The Rejection of Claims 1-9 Under § 101 Should Be Withdrawn Because the Amended Claims Recite Steps that Produce a Concrete, Tangible and Useful Result

The Examiner has maintained a rejection of claims 1-9 for not disclosing statutory subject matter as required by 35 U.S.C. § 101. Specifically, the Examiner asserted that the method of claims 1-9 merely rearranges previously provided data. In response, Applicants have amended independent claims 1 and 7 so that they recite a method that clearly goes beyond rearranging data and provides a concrete, tangible and useful result. Significantly, claim 1 has been amended to clarify a key structural feature of the database, that "the information in any of the data types may be accessed through a query in any other data type." The claimed method then teaches a series of cross-data type analysis steps to be carried out by a user interacting with this database structure that ultimately provides a useful output of "product information." Although this "product information" was previously stored in the database, its specific utility would not be recognized by the user without the cross-data type analysis method taught by amended claims 1-9. The ability of the claimed method to identify a specific useful subset of product information data in a large dataset constitutes a concrete, tangible and useful result that fulfills the statutory subject matter requirement of 35 U.S.C. § 101.

The Rejection of Claims 1-3, 5-8 and 10-16 Under § 102(e) Should Be Withdrawn Because Bassett Jr. *et al.* (US 6,453,241 B1) Does Not Anticipate the Amended Claims

The Examiner has rejected claims 1-3, 5-8, and 10-16 as anticipated under 35 U.S.C. § 102(e) by the Bassett Jr. reference. Bassett Jr. discloses a method and system for analyzing "biological response data" that includes a database of gene expression profiles for a variety of cell types. Bassett Jr. discloses gathering the expression profiles from a variety of experimental techniques that measure expression levels (e.g. SAGE, Northern blot, Lynx, PCR, etc.). Bassett Jr. also discloses obtaining the expression profiles from cells that have been exposed to a variety of perturbations including exposure to drugs. Bassett Jr. teaches a biological response signal database limited to the following types of biological state measurements (see e.g. at Cols. 25, 31 and 32) : (1) "transcriptional state" (i.e. mRNA abundances); (2) "translational state;" (i.e.

protein abundances) (3) "activity state;" (i.e. protein activities relevant to characterization of drug action) and (4) "mixed aspects" (i.e. combinations of transcriptional, translational and protein activity measurements). Bassett Jr. teaches the use of biological comparison algorithms to correlate similar expression profiles within the same type of specific biological response signals (see, e.g. at Col. 14).

The present invention is directed to methods and systems for analysis of chemical genomic information. The present application teaches methods and systems based on a correlative database of chemical genomic data that allows a user to explore previously unknown relationships between genes, expression profiles, compounds, and bioassay data. Furthermore, the present application discloses a database method and system that provides information regarding products useful for further investigating the newly discovered relationships between genes, expression profiles, compounds, and bioassay data. Importantly, it is the database structure that allows access through various different entry points (see e.g., specification at page 9, lines 22-page 10, line 25) and thereby facilitates correlation of chemical genomic information across different data types (see e.g., database structure shown in Fig. 1). Thus, the database allows a user to begin an analysis with a query based on any data type (e.g. gene or pathway, an expression profile, a compound structure, or data from a bioassay) and end up with an unexpected insight and hypothesis that may be tested through an experiment involving a completely different data type. Often the analysis of chemical genomic information using the database systems and methods of the present application will involve a pathway of multiple correlations across data types. It is a surprising result of the present invention that the correlations across data types made possible by the chemogenomic database result in the emergence of chemical and biological insights that may otherwise not be recognized. Further, because it includes product information, the final step of any analysis using the database may include a list of assays and reagents useful to confirm a hypothesis that cannot be answered based on the chemogenomic information provided by the database.

For example, one may query with bioassay information (e.g. compound treatments that cause decreased blood serum albumin levels at a dosage of X mg/kg body weight in rats), display a list of the compounds that yielded those bioassay results, display a list of correlated compounds

(e.g., based on structural similarity) but not tested for their effect on blood serum albumin level, display correlated expression profiles for these correlated compounds, further correlate and display the genes downregulated by these correlated compounds but in a different tissue (e.g. kidney rather than liver), and thereby discover a set of off-target pathways that may be a source of toxic renal side effects for a class of compounds being developed. Further, because it includes product information, the final step of the above investigation may be the display of a list of reagents that may be used to carry out a diagnostic assay to confirm hypothesized side effect (e.g. a set of oligonucleotides useful as probes on an array).

Bassett Jr. does not anticipate the currently amended claims because the reference does not teach or suggest a database method or structure allowing a pathway of correlations to be made across data types in the database. The database described by Bassett Jr. appears to be relatively limited to biological response data consisting of gene expression profile data from cell-based perturbation studies. For example, the database described by Bassett Jr. does not appear to include the range of bioassay data of the present application or results of *in vivo* studies of the standard compounds. Significantly, Bassett Jr. does not appear to teach a method wherein the database may be accessed and queried through any of the multiple data types, or wherein correlation information is determined across multiple different data types. The database analysis methods taught by Bassett Jr. appear to be limited to comparing the expression profile data from different cells perturbed under different conditions. The biological comparison algorithms (e.g., ROAST and FINISH) described by Bassett Jr. appears to be limited to queries based on expression profile data and output that consists of correlation of similar expression profiles (see, e.g., Bassett Jr. at Col. 14, line 14 - Col. 15, line 4).

Furthermore, Bassett Jr. does not teach a database method that includes selecting product information. Regarding the Bassett Jr. disclosure, the Examiner asserts that "Information about the drug (structure, dosage, etc.) and its effects (biological activity) are provided (meeting the limitations of claims 13-16 for display of product information that is related to testing)." Applicants respectfully disagree. "Product information" in the context of the present application refers to a separate category of information regarding the availability, characteristics, price of a product. The "product" refers to an item that may be used to further explore a hypothesis

generated based on a query of the database, for example, a bioassay kit, a DNA microarray, compounds useful as positive or negative controls, protein purification kits, antibodies, etc. The database system described by Bassett Jr. nowhere describes providing this type of information.

The Rejection of Claims 4 and 9 Under § 103(a) Should Be Withdrawn Because Bassett Jr. *et al.* Combined with Pati *et al.* (US 2002/0032530) Does Not Render Obvious Amended Claims

The Examiner has rejected claims 4 and 9 as rendered obvious in view of the Bassett Jr. reference combined with the Pati reference. As stated above, Applicants have now amended the base independent claims 1 and 7 so that they recite an invention no longer anticipated by the Bassett Jr. reference. In light of the these amendments, Applicants respectfully assert that the combination of Bassett Jr. and Pati no longer renders dependent claims 4 and 9 obvious.

CONCLUSION

Applicants believe that the application is in good and proper condition for allowance. If, in the opinion of the Examiner, a telephone conference would expedite the prosecution of the subject application, the Examiner is encouraged to call the undersigned at (650) 463-8133.

Respectfully submitted,

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